

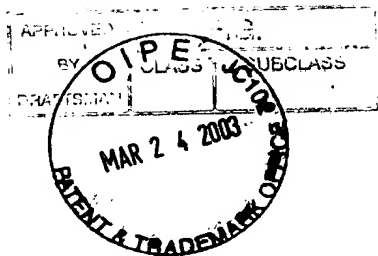


Fig. 1A

TECH CENTER 1600/2900

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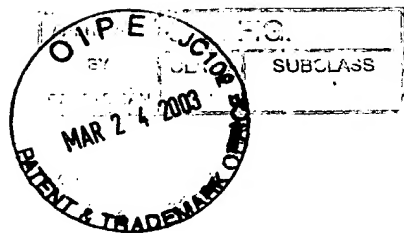
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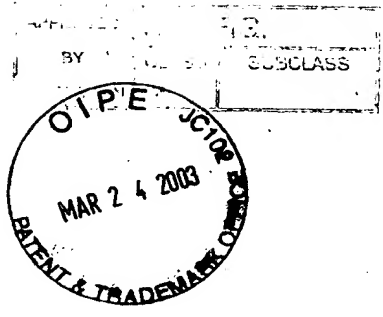
Fig. 1B



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p16EX1	<	GGNGGNAAGNTGTGGGGGAAAGTTTGGGGATGGAANACCAANCCCTCCTTTTCNTTACCAA	60
	+.....+.....+.....+.....+.....+.....+	
p16EX1	<	ACNCTGGCTCTGNCGAGGCTNCNTCCGANTGGTNCCCCGGGGGAGACCCAACCTGGGNC	120
	+.....+.....+.....+.....+.....+.....+	
p16EX1	<	GACTTCAGGGNTGCNACATTCACTAAGTGCTNGGAGNTAATANCACCTCCTCCGAGCANx	180
p16EX13	<	TCNCTTATTGNTAGGANATAATAAacACCTCCACcGATAAACT	41
	+.....+.....+.....+.....+.....+.....+	
p16EX1	<	TCGCTCACAGCGTCCCCTTACCTNGANAGATACCNCGxGxTCCCTCCAGAGGATTTGAGG	240
p16EX13	<	TcaCTTACAACGTCCCNNTtCCTGgaAAGATACacaGCGTTCCTCCAGAGGATTTGTGG	101
	+.....+.....+.....+.....+.....+.....+	
p16EX1	<	GACAGGNTCGGAGGGGGCTCTTCCCCCANACCGGAGGAAGAAAGAGGAGGGNCTGACTG	300
p16EX13	<	GACAGGGTNGGAGNGGTCTCTTCNCNCCACCACCGGAGGAAGAAAGAGGAGGGGCTGNCTG	161
	+.....+.....+.....+.....+.....+.....+	
p16EX1	<	GTCACCAGAGGGTGGGACGGACCGCGTGCGCTCGGCGNCTNCGGAGAGGGGGAGAACAGA	360
p16EX13	<	TTcACCAGAGGGTGGGACGGACCNCGTACGCTCGNCGNCTNCGGAGAGGGGGAGAGCAGT	221
	+.....+.....+.....+.....+.....+.....+	
p16EX1	<	CAACGGGCGGGCGGGAGCAGCATGGATCCGGCGGGGAGCAGCATGGANCCTTCGACT	420
p16EX13	<	CANCGGNCGNCGGGGAGCAACATGGAACCGNCGGGCGGGAGCAGCATGGANCCTTCGGCT	281
	+.....+.....+.....+.....+.....+.....+	
P16NT2	<	GACNNNCTCCGGCCGGNGTCGGGTAGAGGAGGTGCGGGCGCTGCTGGAG	49
p16EX1	<	GACTGACTGCCTCGC	435
p16EX13	<	GACTGGCTGNCCACGNCCACGNCCCAGGGTTCGGGTAGAGGAGGTGCGGNCGCTNCTGGAG	341
	+.....+.....+.....+.....+.....+.....+	
P16NT3	>	GTCTNANCCCGGGTA	15
P16NT2	<	GCGGGGGCGCTGCCCAACGCACCGAATAGTTACGGTTCGGAGGCCGATCAGGTxxGGGTA	109
p16EX13	<	GCGGGGNCTCTGNCCAACNCGCTAAAAAN	369
	+.....+.....+.....+.....+.....+.....+	
P16NT3	>	GAGGGTCTGCAGCGGGAGCAGNGGATGGCGGGCGACTCTGGAGGACGAAGTTTGCAGGGG	75
P16NT2	<	GAGGGTCTGCAGCGGGAGCAGGGGATGGCGGGCGACTCTGGAGGACGAAGTTTGCAGGGG	169
	+.....+.....+.....+.....+.....+.....+	
P16NT3	>	AATTGGAATCAGGTAGCGCTTCGANTCTCCGGAAAAAGGGGAGGCTTCCTGGGGAGTTNN	135
P16NT2	<	AATTGGAATCAGGTAGCGCTTCGATTCTCCNGAAAAAGGGGAGGCTTCCTGGGGAGTTTT	229

Fig. 2A



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.....+.....+.....+.....+.....+.....+
> CAGAAGGGGTTTGTAAATCACAGNCCTCCNCCTGGCGACGCCCTGGGGGGTTGGGAAGCCA 195
< CAGAAGGGGTTTGTAAATCACAGACCTCCTCCTGGCGACGTCCTGGGGGCTTGGGAAGCCA 289

.....+.....+.....+.....+.....+.....+
> AGGAAGAGGAATGAGGAGNCACGCGCNTACAGNTCTCTCGAATNCTGANAAGATCTGAAG 255
< AGGAAGAGGAATNAGGAGCCACGCGCGTACAGATCTCTCGAATGCTGAGAAGATCTNAAG 349

.....+.....+.....+.....+.....+.....+
> GGGGGAACATATTTGTATTAGxATNNAAGTATGCTCTTTATCAGATACAAAATTCACGAA 315
< GGGGGAACATATTTGTATTAGCNTCCAAGTNTNCTCTNTATCANATACAAANTxC 404

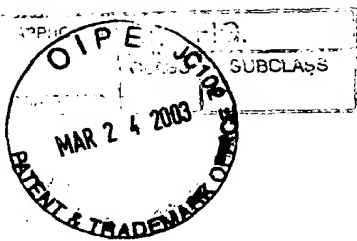
.....+.....+.....+.....+.....+.....+
> CGTGTGGNATAAAAAGGGAGTCTTAAAGAAATNTAAGATGTGCTGGGACTACTTAGCCTC 375

.....+.....+.....+.....+.....+.....+
> CAANACACAGATNCCTGGATGGAGCT 401

.....+.....+.....+.....+.....+.....+
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Fig. 2B

Fig. 2C

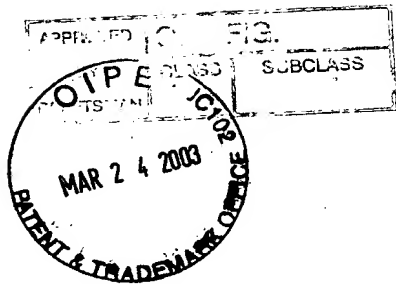


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p16EX5 < xAAGTATGAGCGAAACNAATTGTGGTTTGAGAANAGGNAATCGTAGGGAACTTCGGGATC 60
.....+.....+.....+.....+.....+.....+.....+
p16EX5 < CCNCNGGGANCNCAGAACCTGAGNCGCCNATTGGAAATNACAACTGNCTGNATCACTC 120
.....+.....+.....+.....+.....+.....+.....+
p16EX5 < CGNACCAGGTNCAAAAGATACCTGGGGANGCGGGAAGGAAAGACNACATCNAGACCGCC 180
p16EX9 < CCCC 4
.....+.....+.....+.....+.....+.....+.....+
p16EX5 < TTCGCNCCTXGGNATTGTGAGCAGCCTCTGAGACTCATTXATATNACACTCGTXXXXCTT 240
p16EX9 < ATCGCGCCTTGGGANITGTGAGCNACCATTGAGACTCATNAATATAGCACTCGTTTTTCTT 64
.....+.....+.....+.....+.....+.....+.....+
p16EX5 < CTTACAACCCTGCGGNCCGCGCGGTTCGCGCTTTCTCTGCCCTCCGCCGGGTGGACCTGGA 300
p16EX9 < CTTGCAACCCTGCGGNCCGCGCGGTTCGCGCTNTCTCTGCCCTCCGCNGGGTGGACCTGGA 124
.....+.....+.....+.....+.....+.....+.....+
p16EX5 < GCGCTTGAGCGGTTCGCGCGCCTGGAGCAGCCAGGCGGNCAGTGGACTAGCTGCTGGACC 360
p16EX9 < GCGCTTGAGCGGTTCGCGCGCNCCTGGANCAGCCAGGCGGGCAGTGGACTACCTNCTGGACC 184
.....+.....+.....+.....+.....+.....+.....+
p16EX5 < AGGGAGGTGTGGGAGAGCGGTGGCGCGGGTACATGCACGTGAAGCCATTGCGGAGAACTT 420
p16EX9 < AGGGAGGTGTGGGAGAGCGGTGNCGGCGGGTACATGCACGTGAAGCCATTGCGGAGAACTT 244
.....+.....+.....+.....+.....+.....+.....+
p16EX5 < TATCCATAAGTATTTCAATACCGGTAGGGACGGCAAGAGAGGAGGGCGGGATGTGCCACA 480
p16EX9 < TATCCATAAGTATTTCAATGCCGGTAGGGACGGCAAGAGAGGAGGGCGGGATGTNCCACA 304
.....+.....+.....+.....+.....+.....+.....+
p16EX5 < CATCTTTGACCTCAGGTTTCTAACGCCCTGTTTTCTTTCTGCCCTCTGCAGACAACCCCGA 540
p16EX9 < CATCTTTGACCTCAGGTTTCTAACGCCCTGTTTTCTTTCTGCCCTCTGCAGACATCCCGA 364
.....+.....+.....+.....+.....+.....+.....+
p16EX4 > AGAAATTAGATCATCAGTCACCGATG 26
p16EX5 < TTGAAAGAACCAGAGAGGCTCTGAGAAACC 570
p16EX9 < TTGAAAGAACCAGAGAGGCTCTGAGAAACCTCCGGAACCTTAGxTCATCAxTCGCCGNAA 424
.....+.....+.....+.....+.....+.....+.....+
p16EX4 > GTCCTACAGGGNCACAACCTGNCCCCGCCACAACCCACCCCGNTTTCGTAGTTTTCATTTA 86
p16EX9 < AA 426
.....+.....+.....+.....+.....+.....+.....+
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Fig. 3A

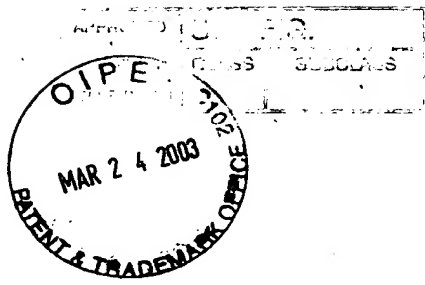
Fig. 3B



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p16EX6	> GNGGATTGGNCCACTACGCNTANCC	503
p16EX6a	> GNGGATTGGNCCACTACGCNTANCCATCACCCCTATTC	515
+.....+.....+.....+.....+.....+	

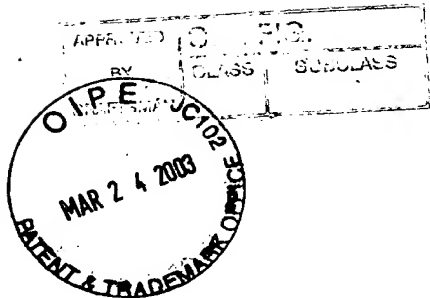
Fig. 3C



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H9	U18	CCL119	MCF-7	HTB 125	SaOs2	A431	NORMAL #1	NORMAL #2	CELL
ABSENT	ABSENT	ABSENT	ABSENT	ABSENT	ALTERED	ALTERED	NORM	NORM	EXON 1
ABSENT	ABSENT	ABSENT	ABSENT	ABSENT	ALTERED	ABSENT	NORM	NORM	EXON 2
W138	CCL120	HeLa	HTB100	ZRB75	GM130	Tera2	HTB172	HTB173	CELL
NORM	NORM	NORM	NORM	NORM	NORM	NORM	NORM	NORM	EXON 1
NORM	NORM	NORM	NORM	NORM	NORM	NORM	NORM	NORM	EXON 2

Fig. 4



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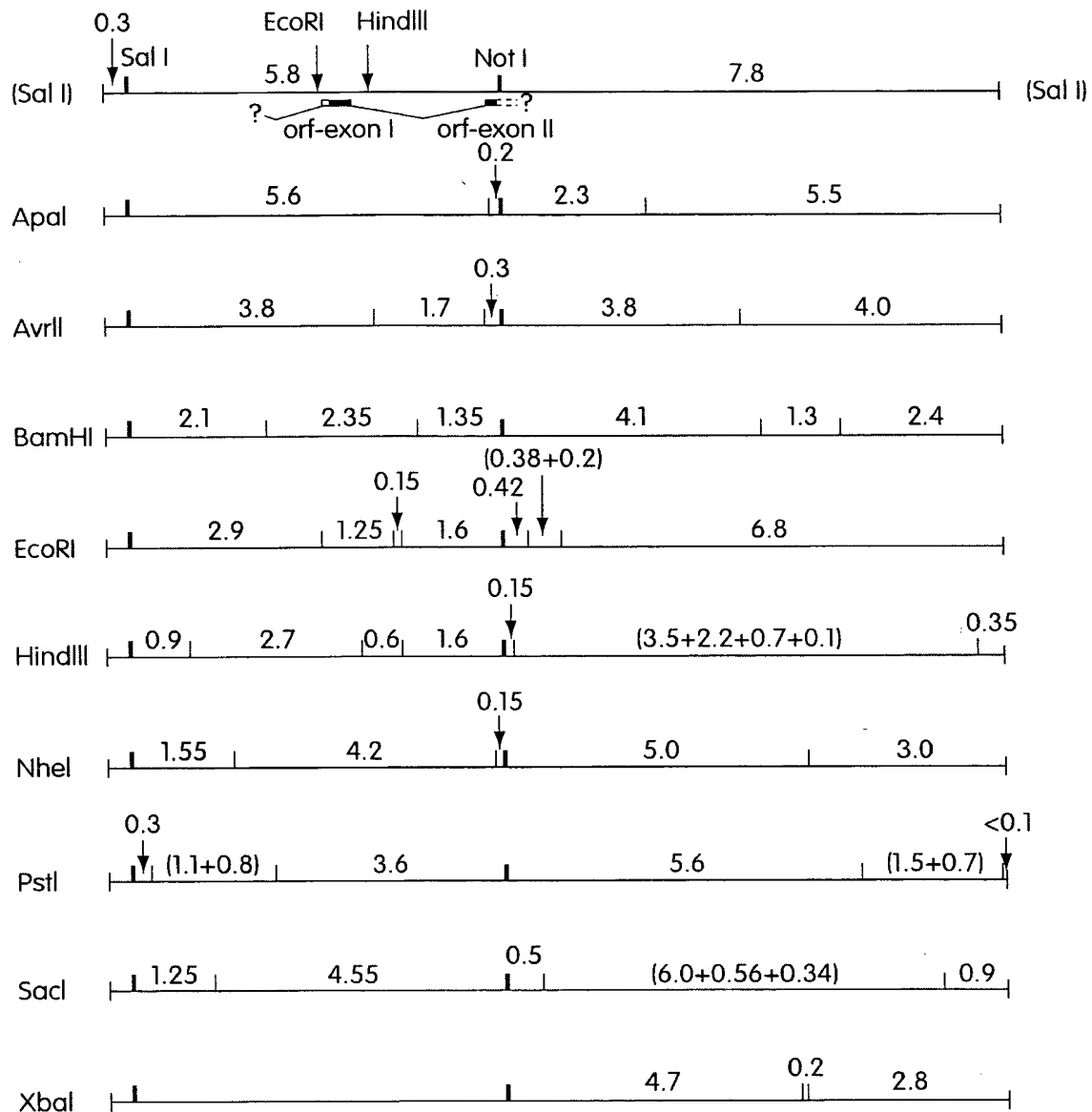
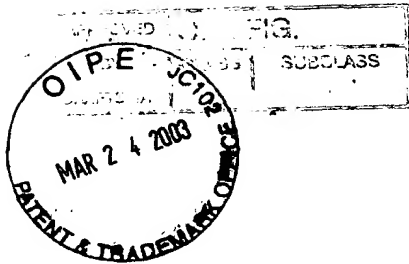


Fig. 5



p16: Ile Gln Val Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala
p15: Ile Gln Val Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala
p13: Met Met Met Gly Asn Val His Val Ala Ala Leu Leu Leu Asn Tyr Gly Ala Asp Ser Asn Cys Glu Asp Pro *

Thr Leu * Thr Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly Ala Arg
Thr Leu * Thr Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly Ala Arg
Thr Thr Phe Ser Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Gly Ser Gly Ala Arg
Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg
Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu Leu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Arg
Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Leu Asp Leu Ala Gln Glu Arg Gly His Gln Asp Ile Val Arg Tyr Leu Arg

Ala Ala Ala Gly Gly Thr
Thr Ala Thr Gly Asp
Ser Ala * Gly Cys Ser

Fig. 6